Insert the attached new page 6 for the originally-filed copy of page 6.

Delete the paragraph spanning page 15, lines 14-24 and insert the following therefor.

Also included within the present invention are sequence variants of the polynucleic acids as selected from any of the nucleotide sequences as given in any of the above given SEQ ID numbers with said sequence variants containing either deletion and/or insertions of one or more nucleotides, especially insertions or deletions of 1 or more codons, mainly at the extremities of oligonucleotides (either 3' or 5'), or substitutions of some non-essential nucleotides (i.e. nucleotides not essential to discriminate between different genotypes of HCV) by others (including modified nucleotides and/or inosine), for example, a type 1 or 2 sequence might be modified into a type 7 sequence by replacing some nucleotides of the type 1 or 2 sequence with type-specific nucleotides of type 7 as shown in for instance ~~Table 6 and 7~~ Figure 1 and 2.

Delete the paragraph spanning page 16, lines 18-22 and insert the following therefor.

Polynucleic acid sequences of the genomes indicated above from regions not yet depicted in the present examples, figures and sequence listing can be obtained by any of the techniques known in the art, such as amplification techniques using suitable primers from the sequences of these new genomes given in ~~Table 6~~ Figure 1.

Delete the paragraph spanning page 27, lines 18-32 and insert the following therefor.

With said notation being composed of a letter representing the amino acid residue by its one-letter code, and a number representing the amino acid numbering according to Kato et al., 1990 as shown in Table 1 (see also the numbering in ~~Tables 7, 8 and 10~~ Figures 2, 4 and 6),

or a part thereof which is unique to at least one of the HCV subtypes or types as defined in Table 5, and which contains at least one amino acid differing from any of the known HCV types or subtypes, or an analog thereof being substantially homologous and biologically equivalent to said polypeptide or part thereof.

These unique amino acid residues can be deduced from aligning the new HCV amino acid sequence as given in Figure 3 ~~SEQ ID NO:1-106~~ to all known HCV sequences. An alignment with the new sequences as represented in SEQ ID NO 1 to 106 is given in for instance ~~Tables 7, 8 and 10~~ Figures 2, 4 and 6. It should be clear that the alignments given in these figures may be completed with all known HCV sequences to illustrate that any of the above-given unique residues in indeed unique for at least one of the new HCV sequences of the present invention.

Delete the paragraph spanning page 27, line 33, to page 28, line 11 and insert the following therefor.

Within the group of unique and new amino acid residues of the present invention, unique residues may be found which are specific for the following new types (subtypes) of HCV according to the HCV classification system used in the present invention: type

1 subtype 1d, 1e, 1f or 1g isolates; type 2 subtype 2e, 2f, 2g, 2h, 2i, 2k or 21 isolates; type 3 subtype 3g isolates; type 4 subtype 4k, 4l or 4m isolates; type 7 subtype 7a, 7c or 7d isolates, type 9, type 10 or type 11 isolates. In order to obtain these residues the alignments given in ~~Tables 7, 8 and 10~~ Figures 2, 4 and 6 may be used to deduce the type- and or subtype-specificity of any of the unique residues given above.

For example T190 (detected in subtype 1d) refers to a threomine at position 190 (see ~~Table 7~~ Figure 2). In other sequences only a serine (S190) or exceptionally an alanine (A190 in type 10a) can be detected.

Delete the paragraph spanning page 28, line 27 to page 29, line 1 and insert the following therefor.

The variable region in the core protein (V-CORE in ~~Table 7~~ Fig. 2) has been shown to be useful for serotyping (Machida et al., 1992). The sequence of the type 1 subtype 1d, 1e, 1f or 1g sequence; type 2 subtype 2e, 2f, 2g, 2h, 2i, 2k and 21 sequence; type 3 subtype 3g; type 4, subtype 4k, 4l or 4m sequence; type 7 (subtype 7a, 7c and 7d sequences), 9, 10 or 11 sequences of the present invention show type-specific features in this region. The peptide from amino acid 68 to 78 (V-core region shows the following unique sequence for the sequences of the present invention (see ~~Table 7~~ figure 2):

Delete the paragraphs spanning page 29, lines 15-20 and insert the following therefor.

Five type-specific variable regions (V1 to V5) can be identified after aligning E1 amino acid sequences of the genotypes of the present invention to the genotypes already known, as shown in ~~Table 7~~ Figure 2.

Region V1 encompasses amino acids 192 to 203, this is the amino-terminal 10 amino acids of the E1 protein. The following unique sequences as shown in ~~Table 7~~ Fig. 2 can be deduced:

Insert the attached new pages 30 and 31 for the originally-filed copies of pages 30 and 31, respectively.

Delete the paragraph spanning page 32, lines 21-26 and insert the following therefor.

The present invention particularly relates to any peptide (see below) or polypeptide contained in any of the amino acid sequences as represented in SEQ ID NO 2, 4, 7, 9, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104 or 106 (see Table 5 and Figure 3 ~~SEQ ID NO:1-106~~, Examples section).

Delete the paragraphs spanning page 49, lines 1-21 and insert the following therefor.

~~TABLE CAPTIONS~~ FIGURE LEGENDS

~~Table Captions~~ Figure Legends

~~Table 6~~ Figure 1

Alignment of the nucleotide sequences of the Core/E1 region of some of the isolates of the newly identified types and subtypes of the present invention, with other known prototype isolates of subtypes.

~~Table 7~~Figure 2

Alignment of the amino acid sequences of the Core/E1 region of some of the isolates of the newly identified types and subtypes of the present invention, with other known prototype isolates of subtypes.

Figure 3

Nucleotide and amino acid sequences obtained from the new HCV isolates of the present invention (SEQ ID NO 1 to 106).

~~Table 8~~ Figure 4

Alignment of the amino acid sequences of the Core/E1 region of some of the isolates of the newly identified types and subtypes of the present invention, with other known prototype isolates of subtypes.

~~Table 9~~ Figure 5

Alignment of the nucleotide sequences of the NS5b region of some of the isolates of the newly identified types and subtypes of the present invention, with other known prototype isolates of subtypes.

Delete the paragraph spanning page 50, lines 1-8 and insert the following therefor.

~~Table 10~~ Figure 6

Alignment of the amino acid sequences of the NS5b region of some of the isolates of the newly identified types and subtypes of the present invention, with other known prototype isolates of subtypes.

Delete Tables 6-10 added as additional pages after page 63 in the Preliminary Amendment filed August 31, 1999.

Insert the attached 74 sheets of formal drawings, after the Abstract, in place of any previously-filed drawings.

Insert the attached Sequence Listing in place of all previously filed copies of the Sequence Listing.